CUBICAL HOMOLOGY AND THE TOPOLOGICAL CLASSIFICATION OF 2D AND 3D IMAGERY

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ABSTRACT

There are a number of tasks in low level vision and image processing that involve computing certain topological characteristics of objects in a given image including connectivity and the number of holes. In this note, we combine a new method combinatorial topology to compute the number of connected components and holes of objects in a given image, and fast segmentation methods to extract the objects.

Key words: *Combinatorial topology, feature recognition, cubical homology, segmentation, holes, connnected components.*

1. INTRODUCTION

In this note, we discuss some new developments in combinatorial topology which can have a major impact in the study of key properties of objects extract from images. The key method we will outline here is *cubical homology* which allows one to compute the homology groups of an object which is defined as a collection of cubes precisely in the manner of digitial imagery. Thus one need not extract triangulated simplicial complexes from the data as is necessary in most conventional techniques. The key advantage then is that all the topological information may be extracted from the *original data* with no subsidiary pre-processing such as skeletonization.

An important issue in low level vision is to reduce the raw image data and to construct a more descriptive representation in terms of relevant features, which can be used more effectively by the other levels of processing. The definition and the computation scheme of the relevant features depend on the image type and more specifically the image formation process that has been used (i.e., visible, near visible, radar, monochromatic, multi-spectral). Many algorithms are now routinely used for description and representation such as image thinning, contour filling, and object counting. Topological features of of interest include the Euler number, number of holes, and the number of connected components. For binary images, there have been a number of approaches; see [4] and the references therein. We should note that a number of the common algorithms for computing the Euler number need the preprocessing step using of skeletonization which make them quite sensitive to noise.

Our approach to extracting topological information is a direct application of the cubical homology and relative homology concepts. Homology theory is well known in the domain of algebraic topology. It is related to the notion of connectivity in multi-dimensional shapes. The classic algorithm for the computation of homology that encodes the complete information about all homology groups of a given complex is based on standard row and column operations on the so-called boundary matrices. Unfortunately, its implementation yields exponential bounds on the worst-case complexity. The high computational cost and the algebraic formulation of homology based on triangulations is of course a major disadvantage in using such topological techniques in computer vision and image processing. However, recent developments in combinatorial homology, the introduction of cubical homology theory and the progress made in designing computer programs computing homology of spaces make it now possible to do this computation in a very easy and suitable way since by essence an image is a cubic grid in the plane and no further triangulation is needed. These points will be elucidated below.

2. COMBINATORIAL TOPOLOGY

Here we briefly outline some key ideas in combinatorial topology and cubical homology theory; for details see [1, 7]. Homology groups are topological invariants which provide an efficient algebraic tool for determining the global shape properties of a given topological space without visualization. This algebraic framework counts the number of holes of all dimensions in a topological space. For a space $X \subset \mathbf{R}^3$, the situation is fairly intuitive since the holes are gaps in dimension 0, independent tunnels in dimension 1, and independent voids in dimension 2. Their number are given by the Betti numbers β_0, β_1 and β_2 of the three possibly

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non-trivial homology groups $H_0(X)$, $H_1(X)$ and $H_2(X)$ associated to the space X. This corresponds to the number of connected components in dimension 0, the number of generic loops in dimension 1, and the number of shells in dimension 2.

There are many different ways of defining homology groups of a topological space. In the standard development, we usually assume that the topological space is given in terms of a particular triangulation or a cell complex. Then one extracts the combinatoric and algebraic information from this structure and frame it as a chain complex [7].

3. CUBICAL HOMOLOGY

Many problems from numerical computations, graphics and computer vision lead naturally to cubical grids subdividing the space into cubes with vertices in an integer lattice. This cubical structure has already enough combinatorial properties to define a homology theory. In computer vision, for example, the standard discretization of an image is achieved via a cubic tessellation. This leads to a complex of unit squares commonly called *pixels*. Any two pixels are either disjoint or intersect through a common edge or a common vertex. The simplicial theory would require subdividing each pixel into union of two triangles and hence increasing the complexity of data. But the approach using cubical homology theory will deal directly with this cubical structure. Another nice feature of the cubical approach is the fact that one does not need to define an orientation on cubes while this notion is essential in the definition of simplicial homology. Indeed, the definition of a cube as a product of intervals in a certain order and the natural order of real numbers imposes an orientation on each coordinate axis and also on the canonical basis of $\mathbf{R}^n$.

The first step for defining cubical homology is to introduce the notion of a *cubical complex* which is in essence exactly the same as of a simplicial complex described before, except one deals with cubes instead of simplices. An *elementary cube* $\sigma \subset \mathbf{R}^n$ is by definition a product

$$\sigma = I_1 \times I_2 \times \cdots \times I_n \tag{1}$$

where I_j is either a singleton or an interval of unit length with integer endpoints, i.e., I_j is either the singleton $\{k\}$, then it is said to be a *degenerate* interval, or the closed interval $[k, k+1]$ for some integer k. The number $q \in \{0, 1, \ldots, n\}$ of nondegenerate intervals in formula (1) is by definition the dimension of σ and σ will be called a *q-cube*. The faces and the boundary of a q-cube are defined in the same manner as for a simplex. A *cubical complex* $\mathcal{K}$ in $\mathbf{R}^n$ is a collection of q-cubes where $0 \leq q \leq n$ such that every face of a cube in $\mathcal{K}$ is also in $\mathcal{K}$, and the intersection of any two cubes of $\mathcal{K}$ is either empty or a face of each of them.

Given a topological space $X \subset \mathbf{R}^n$ in terms of a cubical complex, we define $C_q(X)$ to be the free abelian group generated by all the q-dimensional elementary cubes in X. Thus the elements of this group, called *q-chains* are formal linear combinations of elementary q-cubes. We put $C_q(X) = 0$ if $q < 0$ or $q > n$.

The *boundary map* $\partial_q : C_q(X) \to C_{q-1}(X)$ is a group homomorphism defined on every elementary q-cube as an alternating sum of its $(q-1)$-dimensional faces and extended by linearity to all q-chains. Note that $\partial_0 = 0$ since $C_{-1}(X) = 0$. The boundary map satisfies the very important property

$$\partial^2 = 0\,, \tag{2}$$

i.e., $\partial_q \circ \partial_{q+1} = 0$ for all q. Proofs of these facts are given in [7]. As for a simplicial complex of dimension n, the algebraic information extracted from the given cubical structure can be expressed as a finitely generated free *chain complex* $(\mathcal{C}, \partial)$

$$0 \xrightarrow{\partial_{n+1}} C_n(X) \xrightarrow{\partial_n} \ldots \xrightarrow{\partial_{k+2}} C_{k+1}(X) \xrightarrow{\partial_{k+1}} C_k(X)$$

$$\xrightarrow{\partial_k} C_{k-1}(X) \xrightarrow{\partial_{k-1}} \ldots C_0(X) \xrightarrow{\partial_0} 0.$$

A chain $z \in C_q(X)$ is called *cycle* or, more precisely, *q-cycle* if $\partial_q z = 0$. A chain $z \in C_q(X)$ is called *boundary* if there exists $c \in C_{q+1}(X)$ such that $\partial_{q+1} c = z$. The set of all q-cycles is the subgroup $Z_q := \operatorname{Ker} \partial_q$ of $C_q(X)$ while the set of all boundaries is the subgroup $B_q := \operatorname{Im} \partial_{q+1}$. Equation 2 implies that $\operatorname{Im} \partial_{q+1} \subset \operatorname{Ker} \partial_q$ and hence the quotient group $H_q(X) := \operatorname{Ker} \partial_q / \operatorname{Im} \partial_{q+1}$, called the q-th *cubical homology group* of X is well defined and has the same interpretation as the simplicial homology groups [7]. Moreover, one can remark that the cubical set X considered here can be triangulated and its simplicial homology is isomorphic to the cubical homology of X defined above. Thus, the two theories are equivalent for cubical sets.

The *homology type* of X (also of $(\mathcal{C}, \partial)$) is by definition the sequence of abelian groups

$$H(X) = H(\mathcal{C}) := \{H_q(X)\},\ \ q = 0, 1, 2, \ldots.$$

4. REDUCTION ALGORITHM

Our computational method for determining the homology groups is based on a reduction process of the size of the chain complex by local simplification in such a way that the homology is preserved at each step. Because of its importance to our whole computational scheme, we will discuss it in some detail now. Note that the main advantage of this set-up is that these topological invariants can be defined directly in terms of the pixels and voxels of the original image data.

Consider the finitely generated free chain complex $(\mathcal{C}, \partial)$ given by the sequence

$$0 \xrightarrow{\partial_{n+1}} C_n \xrightarrow{\partial_n} \ldots \xrightarrow{\partial_{k+2}} C_{k+1} \xrightarrow{\partial_{k+1}} C_k$$

$$\xrightarrow{\partial_k} C_{k-1} \xrightarrow{\partial_{k-1}} \ldots C_0 \xrightarrow{\partial_0} 0.$$

Without loss of generality, one may assume that a basis E_k of C_k only formed by elementary k-chains is given for each k. *Elementary k-chains* are k-simplices if the chain complex is derived from a simplicial complex or k-elementary cubes in case it is gotten from a cubical complex. We then define for each k a bilinear form $\langle .,. \rangle : C_k \times C_k \longrightarrow \mathbb{Z}$ on generators $u, v \in E_k$ by

$$\langle u, v \rangle = \begin{cases} 1 & \text{if} \quad u = v \\ 0 & \text{otherwise.} \end{cases}$$

The algorithm is based on the following result. Let $m \in \{1, \ldots, n\}$, $A \in E_m$ and $a \in E_{m-1}$ such that a is a proper face of A, i.e., we can write

$$\partial_m A = \lambda a + r, \tag{3}$$

where $\lambda = \pm 1$ and r is the rest of the boundary of A other than a. We perform a local reduction of E_m and E_{m-1} by removing A from E_m and a from E_{m-1} in such a way as to preserve the homology of $(\mathcal{C}, \partial)$. For this purpose, we define a *reduced chain complex* $(\overline{\mathcal{C}}, \overline{\partial})$. We start with defining new bases

$$\overline{E}_k := \begin{cases} E_k & \text{if} \quad k \neq m-1, m \\ E_{m-1} \setminus \{a\} & \text{if} \quad k = m-1 \\ E_m \setminus \{A\} & \text{if} \quad k = m \end{cases}$$

and a sequence $\{\overline{C}_k\}_k$, where $\overline{C}_k$ is a free abelian group generated by $\overline{E}_k$ for each k. The *reduced boundary map* $\overline{\partial}$ is defined on generators as follows.

$$\overline{\partial}_k v := \begin{cases} \partial_k v & \text{if} \quad k \neq m, m+1 \\ \partial_k v - \lambda^{-1} \langle \partial_k v, a \rangle \, \partial_k A & \text{if} \quad k = m \\ \partial_k v - \langle \partial_k v, A \rangle \, A & \text{if} \quad k = m+1. \end{cases} \tag{4}$$

This means that the boundary map is only updated for generators of dimension m which have a in their boundaries and for generators of dimension $m+1$ which have A in their boundaries. One can guarantee that the homology type of the initial chain complex remains unchanged after a one-step reduction in the follwoing sense:

Theorem 4.1 *$(\overline{\mathcal{C}}, \overline{\partial})$ is a finitely generated free chain complex and $H(\mathcal{C}) = \mathcal{H}(\overline{\mathcal{C}})$.*

Note that the one-step reduction can be performed and iterated in any dimension m as long as the choice of A and a satisfying Equation (3) is possible, i.e., as long as $\partial_m^i \neq 0$ and there is no torsion. (This is always true for the type of subspaces of $\mathbf{R}^n$ that we will be considering.) Typically, given a chain complex $(\mathcal{C}, \partial)$ of dimension n, we perform a sequence of one-step reductions first for $m = n$ until we obtain a complex $(\mathcal{C}^{f_n}, \partial^{f_n})$ such that $\partial_n^{f_n} = 0$. Then we do the same for $m = n-1$ starting with the complex $(\mathcal{C}^{f_n}, \partial^{f_n})$ and so on. The last sequence of reductions is performed for $m = 1$ and a final complex $(\mathcal{C}^f, \partial^f) = (\mathcal{C}^{f_1}, \partial^{f_1})$ is obtained.

5. SEGMENTATION USING AREA AND VOLUME MINIMIZING FLOWS

In this section we briefly discuss segmentation using certain minimizing flows. We follow the treament in [6]. The method works in n dimensions but for the sake of concreteness we treat the 3-D case. The general method is based by modifying the Euclidean volume and area by a function which depends on the salient features which we wish to capture. In order to do this, we will need to set up some notation.

Let $\mathcal{S} : [0,1] \times [0,1] \rightarrow \mathbf{R}^3$ denote a compact embedded surface with (local) coordinates (u, v). Let H denote the mean curvature and $\mathcal{N}$ the inward unit normal. Let $\phi : \Omega \rightarrow \mathbf{R}$ be a positive differentiable function defined on some open subset of $\mathbf{R}^3$. The function $\phi(x, y, z)$ will play the role of a "stopping" function, and in work below will be taken to be of the form

$$\phi = \frac{1}{1 + \|\nabla G_\sigma * I\|^2},$$

where $I(x, y, z)$ is the given gray-level image and G_σ is a Gaussian filter. We now modify the infinitesimal area $d\mathcal{S}$ by multiplying by the weight ϕ, $d\mathcal{S}_\phi := \phi d\mathcal{S}$. Then taking first variation of the corresponding modified volume functional, we derive the flow

$$\mathcal{S}_t = \{\phi + \frac{1}{3}\langle \mathcal{S}, \nabla\phi \rangle\}\mathcal{N}. \tag{5}$$

Now the 3D extension of the standard geodesic contour flow [5, 3] may be shown to be

$$\mathcal{S}_t = (\phi H \mathcal{N} - \langle \nabla\phi, \mathcal{N} \rangle)\mathcal{N}. \tag{6}$$

As in [6], we combine the weighted volume and area minimizing flows and write the resulting equation in level set form:

$$\Psi_t = \alpha \left\{ \phi \, \mathrm{div}\left(\frac{\nabla\Psi}{\|\nabla\Psi\|} \right) + \langle \nabla\phi, \frac{\nabla\Psi}{\|\nabla\Psi\|} \rangle \right\} \|\nabla\Psi\| + \frac{1}{3} \, \mathrm{div}\left(\begin{pmatrix} x \\ y \\ z \end{pmatrix} \phi \right) \|\nabla\Psi\|. \tag{7}$$

Note we have to put in a "fudge" factor α in order to get compatible units in the sum on the right side of (7). Obviously the argument extends to hypersurfaces in $\mathbf{R}^n$.

6. COMPUTER EXPERIMENTS

In this section, we give some computer experiments illustrating our results on real data. Code was written for the algorithm in C++ .

For this, we used an MRI data set provided to us by the Surgical Planning Laboratory of Brigham and Women's Hospital. The set consists of a 256 by 256 by 124 volumetric image of the brain. In is important to emphasize that *the homological algorithm allows one to set a minimal and maximal gray levels in studying various structures of interest.* For simplicity, we decided to apply the flow area and length minimizing flow (7) to produce a binary data image in order to verify the correctness of our algorithm. Note that ventricles generally extend out to the brain surface, and internal voids and tunnels can cause a non-trivial topological structure.

In Figure 1 we give one slice of the original data set. We applied our algorithm of course to the entire segmented brain volume. The segmented slice is given in Figure 2. A view of the surface of the segmented brain volume is given in Figure 3. The betti numbers of the *entire segmented volume* which we computed are $\beta_0 = 1$, $\beta_1 = 3$, $\beta_2 = 1$. We believe that this computation on a complicated structure indicates the potential utility of the algorithm. (The computation took about 25 seconds on an Ultra 80 machine.)

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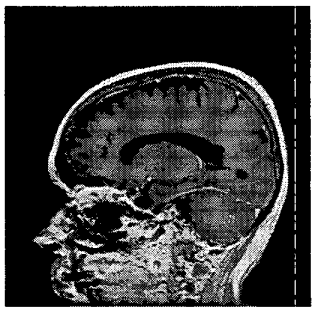

Fig. 1. Original Data Slice

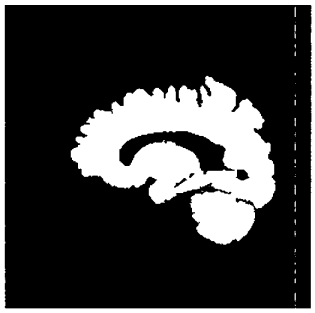

Fig. 2. Segmented Slice

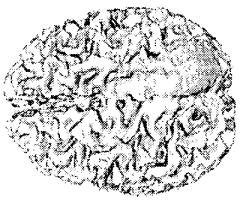

Fig. 3. Surface of Segmented Volume